

Amendments to the Specification:

Please replace paragraph [0056] beginning at page 9, line 14, with the following:

--[0056] A sequence with significant homology to hDGAT2 (40 percent identity at protein level) was identified and named *dgal+* (GeneDB systematic name: SPCC1235.15 (SEQ ID NO:23)). *dgal+* encodes a ~~349-residue~~ 345-residue protein with at least one transmembrane domain. The region of the putative glycerol phospholipid domain in hDGAT2 was also found to be conserved in Dgalp (45% percent identity over 80 amino acids).--

Please replace paragraph [0057] beginning at page 9, line 19, with the following:

--[0057] In addition, as previously reported, an open reading frame highly homologous (45 percent identity at protein level) to the budding yeast LRO1 was found in the fission yeast genome and named *plh1+* (for Pombe LRO1 Homolog 1, GeneDB systematic name: SPBC776.14 (SEQ ID NO:24)). *plh1+* predicts a protein of 623 amino acids, with a putative transmembrane domain near its N terminus. Plh1p also has a conserved serine lipase motif HS(M/L)G between amino acids 292-296.--

Please replace paragraph [0061] beginning at page 10, line 10, with the following:

--[0061] The *dgal+* gene and the *plh1+* gene refer to the *S. pombe* genes that have the sequences identified as GeneDB Accession No. SPCC1235.15 (SEQ ID NO:23) and GeneDB Accession No.SPBC776.14 (SEQ ID NO:24), respectively, or where the yeast strain is other than *S. pombe*, the homologous genes in such other fission yeast strain. The term "homologous" refers to a nucleotide sequence that differs from a reference sequence (here *S. pombe* genes *dgal* or *plh1*) only by one or more conservative substitutions, or by one or more non-conservative substitutions, deletions, or insertions located at positions of the sequence that do not affect the biological function of the translated protein when expressed.--

Please cancel the present "SEQUENCE LISTING", pages 1/6-6/6, submitted for the parent application PCT/SG04/00205, and insert therefor the accompanying paper copy of the Substitute Sequence Listing, page numbers 1-9, at the end of the application.